

REPLACEMENT SHEET

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FIGURE 3 (sheet 1 of 3)

» AHASL1B (1251) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT  
» AHASL1D (945) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT  
» AHASL1A (1058) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT  
(1251)

» CM-F (1) CCGCCGCAATATGCTATCCAG>  
» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG  
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG  
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG  
(1301) +

» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG  
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTTGGG  
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTTGGG  
(1351) + +

» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA  
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA  
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA  
(1401) +

» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTGGGTTGCCAGCTG  
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTGGGTTACCAGCTG  
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTGGGTTACCAGCTG  
(1451) + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT  
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT  
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT  
(1501)

» AHASL1B (1551) GGGGATGGTAGTTTCCTCATGAACATTCAGGAGTTGGCGTTGATCCGTAT  
» AHASL1D (1245) GGTGATGGTAGTTTCCTCATGAACATTCAGGAGTTGGCGTTGATCCGCAT  
» AHASL1A (1358) GGAGATGGTAGTTTCCTCATGAACATTCAGGAGTTGGCATTGATCCGTAT  
(1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA  
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA  
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA  
(1601) +

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**FIGURE 3 (sheet 3 of 3)**

» AHASL1B	(2101)	GAACCGTGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC
» AHASL1D	(1795)	GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC
» AHASL1A	(1908)	GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC
	(2101)	+ + + + +
» AHASL1B	(2151)	ATAARATATCATGCAAGTTTCTTGTCCTACATATCAATAATAAGCACTTC
» AHASL1D	(1845)	ATAARATRTCATGCAAGTTTCTTGTCCTACATATCAATAATAAGTACTTC
» AHASL1A	(1958)	ATAAAATATCATGCAAGTTTCTTGTCCTACATATCAATAATAAGTACTTC
« CM-R	(1)	<u>&lt;&lt;GTACGTTCAAAGAACAGGATG</u>
	(2151)	+ + +
» AHASL1B	(2201)	CATGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1D	(1895)	CATGCAGTAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1A	(2008)	CATGGAAAAAAAAAAAAAAAAAAAAAAAAA
	(2201)	+ ++

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**FIGURE 4 (sheet 1 of 3)**

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» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
(1301) +

» 1AD-F (1) GGGAGGCCATCATTGCCACT>>
» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTGGG
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTGGG
(1351) + +

» 1B-F (1) GGCA
» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
(1401) +

» 1B-F (6) GTGGCTGTCTTCATCC>>
» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTGTTGGGTTGCCAGCTG
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTGTTGGGTTACCAGCTG
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTGTTGGGTTACCAGCTG
(1451) + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
(1501)

» AHASL1B (1551) GGGGATGGTAGTTTCTCATGAACATTCAGGAGTTGGCGTTGATCCGTAT
» AHASL1D (1245) GGTGATGGTAGTTTCTCATGAACATTCAGGAGTTGGCGTTGATCCGCAT
» AHASL1A (1358) GGAGATGGTAGTTTCTCATGAACATTCAGGAGTTGGCATTGATCCGTAT
(1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCCAGCATCTGGGAA
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCCAGCATCTGGGAA
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCCAGCATCTGGGAA
(1601) +

« 1A-R (1)
» AHASL1B (1651) TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
» AHASL1D (1345) TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
» AHASL1A (1458) TGGTGGTGCAATGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
(1651) +

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**FIGURE 4 (sheet 2 of 3)**

» AHASL1B	(1701)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
» AHASL1D	(1395)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
» AHASL1A	(1508)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
	(1701)		
» AHASL1B	(1751)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG	
» AHASL1D	(1445)	GATTGCTAAAGGATTCAACGTTCCAGCAGTTCGAGTGACGAAGAAGAGCG	
» AHASL1A	(1558)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG	
	(1751)		+ +
» AHASL1B	(1801)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
» AHASL1D	(1495)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
» AHASL1A	(1608)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
	(1801)		
» WT-F	(1)		GTGCTGCCTATGATCCGAAG
» MU-F	(1)		CGTGCTGCCTATGATCCGAAC
» AHASL1B	(1851)	TTGGATATCATTTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
» AHASL1D	(1545)	TTGGATATCATAGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
» AHASL1A	(1658)	TTGGATATCATCGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
	(1851)		+ + +
» AHASL1B	(1901)	CGGTGGTGCTTTTAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
» AHASL1D	(1595)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
» AHASL1A	(1708)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
	(1901)		+
» AHASL1B	(1951)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
» AHASL1D	(1645)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
» AHASL1A	(1758)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
	(1951)		
» AHASL1B	(2001)	TGATACCTGCGTGTGTGTATCAACTACTGGGGGTTCAACTGTGAACCATGC	
» AHASL1D	(1695)	TGATGCCCCGCGTGTGTGTATCAACTACTAGGGGTTCAACTGTGARCCATGC	
» AHASL1A	(1808)	TGGTGCCCCGCGTGTGTGTATCAACTACTAGGGGTTCAACTGTGAACCATGC	
« 1B-R	(1)	<b>&lt;&lt;TCGAGGCACAACATAGTTGATGAC</b>	
	(2001)	+ + +	+ +
» AHASL1B	(2051)	GTTTTCTAGTTTGTCTTGTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
» AHASL1D	(1745)	GTTTTCTAGTTTGTCTTGTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
» AHASL1A	(1858)	GTTTTCTAGTTTGTCTTGTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
	(2051)		+

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**FIGURE 4 (sheet 3 of 3)**

» AHASL1B	(2101)	GAACCGTGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC
» AHASL1D	(1795)	GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC
» AHASL1A	(1908)	GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC
« 1D-R	(1)	<<TAGAAGAGAAAACATCCCTACAG
« 1A-R	(1)	<<GATAGAAAACATCCCTACAGACAG
	(2101)	+ + + ++ + +
» AHASL1B	(2151)	ATAARATATCATGCAAGTTTCTTGTCTTACATATCAATAATAAGCACTTC
» AHASL1D	(1845)	ATAARATRTCATGCAAGTTTCTTGTCTTACATATCAATAATAAGTACTTC
» AHASL1A	(1958)	ATAAAATATCATGCAAGTTTCTTGTCTTACATATCAATAATAAGTACTTC
	(2151)	+ + +
» AHASL1B	(2201)	CATGGAGCAAAAAAAAAAAAAAAAAAAAAA
» AHASL1D	(1895)	CATGCAGTAAAAAAAAAAAAAAAAAAAAA
» AHASL1A	(2008)	CATGGAAAAAAAAAAAAAAAAAAAAA